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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/462,846

DATE: 02/02/2001  
TIME: 16:35:53

Input Set : A:\GC381-US-seqlist.txt  
Output Set: N:\CRF3\02022001\I462846.raw

3 <110> APPLICANT: Estell, David A.  
5 <120> TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
8 <130> FILE REFERENCE: GC381-US  
10 <140> CURRENT APPLICATION NUMBER: US 09/462,846  
11 <141> CURRENT FILING DATE: 2000-01-13  
13 <150> PRIOR APPLICATION NUMBER: PCT/US98/19529  
14 <151> PRIOR FILING DATE: 1998-07-14  
16 <150> PRIOR APPLICATION NUMBER: EP 97305227.7  
17 <151> PRIOR FILING DATE: 1997-07-15  
19 <160> NUMBER OF SEQ ID NOS: 7  
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
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24 <211> LENGTH: 945  
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31 gccgcgcata aaaatggta aagcgttgtt caaaaacggaa tgtataaggg gttcacgctc 180  
32 agcgaattat gggAACATCA caacattttt ttcggacagc ttgaaggggg cggtttccct 240  
33 ctgtttacaa aaatatttta tgctgaccag gacttatctg ttcaggtgca tccgaatgtat 300  
34 gaatatgcca acatacatga aaacygttag cttygaaaaa cagaatgtgc gtacattatt 360  
35 gattgccaaa aagatgccc gatttatggccacaatg caacaacaaa ggaaagaacta 420  
36 actaccatga tagacgtgg agaatggat gagtcattgc gccgtgtaaa ggtaaagccg 480  
37 ggggattttt tctatgtgcc aagcggtaact gttcatgcqa ttggaaaaagg aattcttgc 540  
38 ttggagacgc agcagaactc agacacaacc tacagattat atgattatga ccgaaaaagat 600  
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40 tctattcccg aacggcatac agtccaccaatggccacaatgg agatgtgc tacaacgaca 720  
41 ttgattgaat ggccttactt ttccgtgggg aaatggact ttcaggate agcaagctta 780  
42 aagcagcaaa aaccattctc tctatcgtt gtatggaaag gggagggccg tatgtatct 840  
43 ggtgatgtatg tctatccctt caaaaagga gatcatatgt tgctgcctta cggcttgg 900  
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55 20 25 30  
56 Arg Thr Gly Glu Cys Trp Ala Phe Ala Ala His Gln Asn Gly Gln Ser  
57 35 40 45  
58 Val Val Gln Asn Gly Met Tyr Lys Gly Phe Thr Leu Ser Glu Leu Trp  
59 50 55 60  
60 Gln His His Arg His Leu Phe Gly Gln Leu Glu Gly Asp Arg Phe Pro  
61 65 70 75 80

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63 85 90 95
64 His Pro Asn Asp Glu Tyr Ala Asn Ile His Glu Asn Gly Glu Leu Gly
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66 Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Gln Lys Asp Ala Glu Ile
67 115 120 125
68 Ile Tyr Gly His Asn Ala Thr Thr Lys Glu Glu Leu Thr Thr Met Ile
69 130 135 140
70 Glu Arg Gly Glu Trp Asp Glu Leu Leu Arg Arg Val Lys Val Lys Pro
71 145 150 155 160
72 Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Val His Ala Ile Gly Lys
73 165 170 175
74 Gly Ile Leu Ala Leu Glu Thr Gln Gln Asn Ser Asp Thr Thr Tyr Arg
75 180 185 190
76 Leu Tyr Asp Tyr Asp Arg Lys Asp Ala Glu Gly Lys Leu Arg Glu Leu
77 195 200 205
78 His Leu Lys Lys Ser Ile Glu Val Ile Glu Val Pro Ser Ile Pro Glu
79 210 215 220
80 Arg His Thr Val His His Glu Gln Ile Glu Asp Leu Leu Thr Thr Thr
81 225 230 235 240
82 Leu Ile Glu Cys Ala Tyr Phe Ser Val Gly Lys Trp Asn Leu Ser Gly
83 245 250 255
84 Ser Ala Ser Leu Lys Gln Gln Lys Pro Phe Leu Leu Ile Ser Val Ile
85 260 265 270
86 Glu Gly Glu Gly Arg Met Ile Ser Gly Glu Tyr Val Tyr Pro Phe Lys
87 275 280 285
88 Lys Gly Asp His Met Leu Leu Pro Tyr Gly Leu Gly Glu Phe Lys Leu
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94 <211> LENGTH: 220
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103 Cys Trp Ala Phe Ser Ala Val Val Thr Ile Glu Gly Ile Ile Lys Ile
104 35 40 45
105 Arg Thr Gly Asn Leu Asn Glu Tyr Ser Glu Gln Glu Leu Leu Asp Cys
106 50 55 60
107 Asp Arg Arg Ser Tyr Gly Cys Asn Gly Gly Tyr Pro Trp Ser Ala Leu
108 65 70 75 80
109 Gln Leu Val Ala Gln Tyr Gly Ile His Tyr Arg Asn Thr Tyr Pro Tyr
110 85 90 95
111 Glu Gly Val Gln Arg Tyr Cys Arg Ser Arg Glu Lys Gly Pro Tyr Ala
112 100 105 110

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 114 115 120 125  
 115 Leu Leu Tyr Ser Ile Ala Asn Gln Pro Val Ser Val Val Leu Glu Ala  
 116 130 135 140  
 117 Ala Gly Lys Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro  
 118 145 150 155 160  
 119 Cys Gly Asn Lys Val Asp His Ala Val Ala Ala Val Gly Tyr Gly Pro  
 120 165 170 175  
 121 Asn Tyr Ile Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn  
 122 180 185 190  
 123 Gly Tyr Ile Arg Ile Lys Arg Gly Thr Gly Asn Ser Tyr Gly Val Cys  
 124 195 200 205  
 125 Gly Leu Tyr Thr Ser Ser Phe Tyr Pro Val Lys Asn  
 126 210 215 220  
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 136 atttccgcctc atccaaaagg accgagactt gttgcaaattt gcccgtataa aggaaajaca 180  
 137 ttgatcgagc tttggaaaga gcacccgtgaa gtattccggcg qcgttagaggg ggatcggtt 240  
 138 ccgcttctga caaagctgtt ggatgtgaag gaagatacgt caattaaagt tcaccctgtat 300  
 139 gattactatc ccggaaaaaa cgaagggaa gaactccggca agacggaaatg ctggtaacatt 360  
 140 atcgaactgtt agaaaaaacgc agaaatcatt tacgggcata cggcccyctt aaaaaccgaa 420  
 141 ctgttcacaa tgataaacagc cggtgactgg gagggcctgc tgcaagaat caaaattaa 480  
 142 ccgggttattt tctattatgtt gcccggcggaa acgctgcacg catttgtcaaa gggggccctt 540  
 143 gtttttagaga ctcagcaaaa ttcatgttgc acataccggg tttacgatgg tggccgtt 600  
 144 gatagcaacgc gaagtcccgag agacgttcat ttgcggaaacggtcaatgc cgccacgtt 660  
 145 cccccatgtgg acggatatat agatgtatcg acagaatcaa gaaaaggat aaccattaa 720  
 146 acatttgccaaatgggaaata ttttcgggtt tataatggg acatcaatgg cgaagctgaa 780  
 147 atggctcagg atgaatccctt tctgttttgc acgctgtatgg aaggaaagcggtt 840  
 148 tatgaggaca aaacatgttcc gctcaaaaaa ggtgtatcaatgg ttttgcggcc ggtcaatgg 900  
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 160 20 25 30  
 161 Glu Ser Thr Gly Glu Cys Trp Ala Ile Ser Ala His Pro Lys Gly Pro  
 162 35 40 45  
 163 Ser Thr Val Ala Asn Gly Pro Tyr Lys Gly Lys Thr Leu Ile Glu Leu  
 164 50 55 60  
 165 Trp Glu Glu His Arg Glu Val Phe Gly Val Glu Gly Asp Arg Phe

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168	Lys	Leu	Leu	Asp
169	Val	His	Pro	Asp
170	Tyr	Tyr	Tyr	Tyr
171	Ala	Gly	Glu	Asn
172	100	105	110	115
173	Gly	Lys	Thr	Glu
174	Cys	Trp	Tyr	Ile
175	Tyr	Ile	Asp	Cys
176	Arg	Cys	Lys	Glu
177	Asn	Ala	Asn	Ala
178	Asp	Gly	Glu	Asn
179	Tyr	Ile	Val	Thr
180	130	135	140	145
181	Ile	Asn	Ser	Gly
182	Gly	Asp	Trp	Glu
183	Arg	145	150	155
184	Phe	Tyr	Tyr	Val
185	Pro	Val	Pro	Ser
186	Gly	Tyr	Tyr	Gly
187	Thr	Ile	Leu	His
188	Leu	Asp	Arg	Ala
189	165	170	175	180
190	Gly	Ala	Leu	Val
191	180	185	190	185
192	Val	Tyr	Asp	Tyr
193	195	200	205	195
194	Asp	Arg	Leu	Asp
195	Arg	195	200	205
196	Val	Ser	Asn	Gly
197	Asp	Pro	Ser	Pro
198	195	200	205	195
199	Leu	Asn	Asn	Ala
200	Ala	Ala	Ala	Ala
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202	Val	Asp	Val	Asp
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205	Ile	Asp	Glu	Ser
206	Asp	Thr	Glu	Ser
207	Arg	Arg	Arg	Lys
208	225	230	235	225
209	Thr	Phe	Val	Gln
210	Phe	Tyr	Gly	Glu
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212	Val	Gly	Glu	Tyr
213	Gly	Tyr	Phe	Ser
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215	Asp	Glu	Leu	Ile
216	265	270	275	265
217	Met	Ala	Gly	Glu
218	280	285	290	280
219	Ala	Gly	Leu	Leu
220	295	300	295	295
221	Asp	Asp	Ile	Leu
222	His	Phe	Ile	Leu
223	295	300	295	295
224	Pro	Leu	Pro	Ala
225	305	310	315	305
226	Asn	Gln	Asn	Met
227	Met	Pro	Asp	Pro
228	Pro	Asp	Phe	Thr
229	310	315	320	310
230	Asp	Thr	Cys	Pro
231	320	325	330	320
232	Leu	Lys	Tyr	Gly
233	330	335	340	330
234	Asp	Lys	Gly	Asp
235	340	345	350	340
236	His	Phe	Ile	Leu
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238	Leu	Pro	Ala	Gln
239	355	360	365	355
240	Pro	Asp	Phe	Thr
241	360	365	370	360
242	Asn	Asn	Asn	Asn
243	370	375	380	370
244	Met	Pro	Asp	Phe
245	380	385	390	380
246	Pro	Asp	Phe	Thr
247	390	395	400	390
248	Asp	Phe	Thr	Cys
249	400	405	410	400
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252	Thr	Cys	Pro	Asp
253	420	425	430	420
254	Cys	Pro	Asp	Phe
255	430	435	440	430
256	Pro	Asp	Phe	Thr
257	440	445	450	440
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262	Thr	Cys	Pro	Asp
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265	480	485	490	480
266	Pro	Asp	Phe	Thr
267	490	495	500	490
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293	620	625	630	620
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295	630	635	640	630
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309	700	705	710	700
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327	790	795	800	790
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333	820	825	830	820
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341	860	865	870	860
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343	870	875	880	870
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345	880	885	890	880
346	Pro	Asp	Phe	Thr
347	890	895	900	890
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352	Thr	Cys	Pro	Asp
353	920	925	930	920
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359	950	955	960	950
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366	Pro	Asp	Phe	Thr
367	990	995	1000	990
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370	Phe	Thr	Cys	Pro
371	1010	1015	1020	1010
372	Thr	Cys	Pro	Asp
373	1020	1025	1030	1020
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385	1080	1085	1090	1080
386	Pro	Asp	Phe	Thr
387	1090	1095	1100	1090
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389	1100	1105	1110	1100
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393	1120	1125	1130	1120
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409	1200	1205	1210	1200
410	Phe	Thr	Cys	Pro
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412	Thr	Cys	Pro	Asp
413	1220	1225	1230	1220
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415	1230	1235	1240	1230
416	Pro	Asp	Phe	Thr
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419	1250	1255	1260	1250
420	Phe	Thr	Cys	Pro
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422	Thr	Cys	Pro	Asp
423	1270	1275	1280	1270
424	Cys	Pro	Asp	Phe
425	1280	1285	1290	1280
426	Pro	Asp	Phe	Thr
427	1290	1295	1300	1290
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429	1300	1305	1310	1300
430	Phe	Thr	Cys	Pro
431	1310	1315	1320	1310
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222 <211> LENGTH: 315
223 <212> TYPE: PRT
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225 <400> SEQUENCE: 7
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233   50          55          60
234 Lys Asp His Pro Glu Ile Phe Gly Phe Pro Asp Gly Lys Val Phe Pro
235   65          70          75          80
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237   85          90          95
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239   100         105         110
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241   115         120         125
242 Ile Leu Gly His Ala Ser Thr Lys Glu Glu Phe Lys Gln Arg Ile
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244 Glu Ser Gly Asp Trp Asn Gly Leu Leu Arg Arg Ile Lys Ile Lys Pro
245   145         150         155         160
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249   180         185         190
250 Val Tyr Asp Tyr Asp Arg Cys Asn Asp Gln Gly Gln Lys Arg Thr Leu
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258 Arg Ala Ala Phe Pro Ser Tyr Gln Thr Tyr Leu Leu Gly Ser Val Leu
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